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**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/727,084**DATE: 04/11/97  
TIME: 14:08:13

INPUT SET: S16960.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

1                           SEQUENCE LISTING  
2  
3     (1)    General Information:  
4  
5         (i) APPLICANT:       Pulst, Stefan M.  
6  
7         (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR  
8                           ATAXIA-2 AND PRODUCTS RELATED THERETO  
9  
10      (iii) NUMBER OF SEQUENCES: 5  
11  
12      (iv) CORRESPONDENCE ADDRESS:  
13         (A) ADDRESSEE: Pretty, Schroeder & Poplawski  
14         (B) STREET:           444 South Flower Street, Suite 2000  
15         (C) CITY:           Los Angeles  
16         (D) STATE:           CA  
17         (E) COUNTRY:          USA  
18         (F) ZIP:            90071  
19  
20      (v) COMPUTER READABLE FORM:  
21         (A) MEDIUM TYPE:       3.5" diskette  
22         (B) COMPUTER:          IBM PC compatible  
23         (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
24         (D) SOFTWARE:         PatentIn Release #1.0, Version #1.25  
25  
26      (vi) CURRENT APPLICATION DATA:  
27         (A) APPLICATION NUMBER: 08/727,084  
28         (B) FILING DATE:       October 8, 1996  
29         (C) CLASSIFICATION:  
30  
31      (viii) ATTORNEY/AGENT INFORMATION:  
32         (A) NAME:            Viviana Amzel, Ph. D.  
33         (B) REGISTRATION NUMBER: 30930  
34         (C) REFERENCE/DOCKET NUMBER: P07 37217  
35  
36      (ix) TELECOMMUNICATION INFORMATION:  
37         (A) TELEPHONE: 213-622-7700  
38         (B) TELEFAX: 213-489-4210  
39  
40  
41     (2) INFORMATION FOR SEQ ID NO:1:  
42  
43         (i) SEQUENCE CHARACTERISTICS:  
44         (A) LENGTH: 516 base pairs  
45         (B) TYPE: nucleic acid  
46         (C) STRANDEDNESS: both

12  
88,  
**ENTERED**

**RAW SEQUENCE LISTING  
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47                   (D) TOPOLOGY: both

48                   (ii) MOLECULE TYPE: DNA (genomic)

50

51

52

53                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

54

55       TTGGTAGCAA CGGAAACGGC GGCGGCCGT TTGGCCCGG CTCCGGCGG CTCCTGGTC      60

56

57       TCGGCGGGCC TCCCCGCCCC TTCTCGTCTG TCCTTCTCCC CCTCGCCAGC CGGGCGCCC      120

58

59       CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TGCGTCCCCG CGCGTTCGG      180

60

61       GCGTCTCCTT GGCGCGCCCG GCTCCCGGCT GTCCCCGCCC GGCGTGCAGC CGGGTGTATG      240

62

63       GGCCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC      300

64

65       AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA      360

66

67       AGCCGGCGG CAGCGGCCTT CTAGCGTCTG CGCGCCGCCGC GCCTTCGCCG TCCTCGTCCT      420

68

69       CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGCGACC TCCGGCGCG      480

70

71       GGAGGGCCGG CCTGGGCAGG TGGGTGTCTGG CACCCC                                  516

72

73                   (2) INFORMATION FOR SEQ ID NO:2:

74

75                   (i) SEQUENCE CHARACTERISTICS:

76                   (A) LENGTH: 4481 base pairs

77                   (B) TYPE: nucleic acid

78                   (C) STRANDEDNESS: both

79                   (D) TOPOLOGY: both

80

81                   (ii) MOLECULE TYPE: cDNA

82

83

84                   (ix) FEATURE:

85                   (A) NAME/KEY: CDS

86                   (B) LOCATION: 163..4101

87

88

89                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

90

91       ACCCCGAGA AAGCAACCCA GCGGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG      60

92

93       GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG      120

94

95       CACCTCCGCT CCCACCCGGC GCCTCGGCCGC GCGCGCCCTC CG ATG CGC TCA GCG      174

96

Met Arg Ser Ala

1

97

98

99       GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC      222

**RAW SEQUENCE LISTING  
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**INPUT SET: SI6960.raw**

100	Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe	
101	5 10 15 20	
102		
103	GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG	270
104	Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg	
105	25 30 35	
106		
107	CGG AGC GGG CGG GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC	318
108	Arg Ser Gly Arg Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser	
109	40 45 50	
110		
111	GCC GCC CCT CCC CCG CCC GGC CCC CCG CCT CCC TCC CGG CAG AGC	366
112	Ala Ala Pro Pro Pro Gly Pro Gly Pro Pro Ser Arg Gln Ser	
113	55 60 65	
114		
115	TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC	414
116	Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly	
117	70 75 80	
118		
119	GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT	462
120	Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly Pro	
121	85 90 95 100	
122		
123	CCC CGC CCC TTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC	510
124	Pro Arg Pro Phe Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala	
125	105 110 115	
126		
127	CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC	558
128	Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser	
129	120 125 130	
130		
131	CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC	606
132	Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro	
133	135 140 145	
134		
135	CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG	654
136	Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys	
137	150 155 160	
138		
139	CCC CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG	702
140	Pro Gln	
141	165 170 175 180	
142		
143	CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC	750
144	Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn Val Arg	
145	185 190 195	
146		
147	AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GGC GCG CCT TCG	798
148	Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser	
149	200 205 210	
150		
151	CCG TCC TCG TCC TCG GTC TCC TCG TCG GCC ACG GCT CCC TCC TCG	846
152	Pro Ser Ser Ser Ser Val Ser Ser Ser Ala Thr Ala Pro Ser Ser	

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153	215	220	225	
154				
155	GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC AGA GGT			894
156	Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly			
157	230	235	240	
158				
159	CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA			942
160	Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly			
161	245	250	255	260
162				
163	ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC			990
164	Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly			
165	265	270	275	
166				
167	TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT			1038
168	Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val			
169	280	285	290	
170				
171	TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT			1086
172	Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His			
173	295	300	305	
174				
175	GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG			1134
176	Glu Lys Ser Thr Glu Ser Ser Gly Pro Lys Arg Glu Glu Ile Met			
177	310	315	320	
178				
179	GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA			1182
180	Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys			
181	325	330	335	340
182				
183	GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT			1230
184	Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala			
185	345	350	355	
186				
187	ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC			1278
188	Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro			
189	360	365	370	
190				
191	TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA			1326
192	Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Leu Glu Ala Leu Glu			
193	375	380	385	
194				
195	AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT			1374
196	Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn			
197	390	395	400	
198				
199	GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG			1422
200	Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser			
201	405	410	415	420
202				
203	TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG			1470
204	Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg			
205	425	430	435	

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206	GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT GCC CAG	1518
207	Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln	
208	440 445 450	
209		
210		
211	TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA	1566
212	Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu	
213	455 460 465	
214		
215	AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC	1614
216	Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser	
217	470 475 480	
218		
219	ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA	1662
220	Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg	
221	485 490 495 500	
222		
223	GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC	1710
224	Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly	
225	505 510 515	
226		
227	CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA	1758
228	Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser	
229	520 525 530	
230		
231	GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT GGA GGT	1806
232	Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn Gly Gly	
233	535 540 545	
234		
235	GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA CCT TCT	1854
236	Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Arg Pro Pro Ser	
237	550 555 560	
238		
239	CGC TAC CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC ACC CCT	1902
240	Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala Thr Pro	
241	565 570 575 580	
242		
243	ACA CGG CCG CCC TCC AGG CCC CCC TCG CGG CCA TCC AGA CCC CCG TCT	1950
244	Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro Pro Ser	
245	585 590 595	
246		
247	CAC CCC TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG CCT AAA	1998
248	His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met Pro Lys	
249	600 605 610	
250		
251	CGC ATG TCT TCA GAA GGG CCT CCA AGG ATG TCC CCA AAG GCC CAG CGA	2046
252	Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala Gln Arg	
253	615 620 625	
254		
255	CAT CCT CGA AAT CAC AGA GTT TCT GCT GGG AGG GGT TCC ATA TCC AGT	2094
256	His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Ile Ser Ser	
257	630 635 640	
258		

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**SEQUENCE VERIFICATION REPORT  
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Original Text